C9 amended was detected using the DELFIA™ system, the downstream primer was biotinylated at the 5' end to allow specific capture of amplified sequences through the use of streptavidin.

Please replace the paragraph at page 28, lines 3-13 with the following:

C10 **Southern Blotting:** Standard southern blotting techniques were used to confirm the PCR results (Tables 2 and 3). Following agarose gel electrophoresis, PCR products were transferred to Hybond N+ membranes (Amersham, Live Science, Arlington Heights, IL). Amplification of human-*P. carinii MSG* was detected using probe JKK16 (SEQ ID NO: 19), which corresponds to residues of 2926-2950 of *HMSG33*. Amplification of *P. carinii* MRSU was detected using pAZ102-L2 (Wakefield *et al.* (1990) *Mol. and Biochem. Parasitol.* 43:69-76). Oligonucleotides were labeled with [γ-^{32}P]-ATP by T4 polynucleotide kinase (Ready-to-Go™ Molecular Biology Reagents, Pharmacia Biotech, Denmark). Prehybridization and hybridization were performed overnight at 52° C in 6 X SSPE, 1% sodium dodecyl sulfate (SDS), 10 X Denhardts' solution (Research Genetics, Huntsville, Alabama). Filters were washed at 52° C in 1 x SSPE, 0.5% SDS for 30 min, then 0.1 x SSPE, 0.5% SDS for 15 minutes.

In the Claims:

Please amend the claims to read as follows:

C11 1. (**amended**) A method of detecting the presence of *Pneumocystis carinii* in a human biological specimen, comprising:

amplifying a highly conserved region within a human-*P. carinii* nucleic acid sequence, if such sequence is present in the specimen, using two or more oligonucleotide primers that hybridize to the highly conserved region; and

determining whether an amplified sequence is present,

wherein the highly conserved region has at least 79% sequence identity with residues 2794-3042 of *HMSGp1* (SEQ ID NO: 1), 2758-3006 of *HMSGp3* (SEQ ID NO: 3), 2845-3090 of *HMSG11* (SEQ ID NO: 5), 2839-3084 of *HMSG14* (SEQ ID NO: 7), 2836-3081 of *HMSG32* (SEQ ID NO: 9), 2809-3054 of *HMSG33* (SEQ ID NO: 11), or 1-249 of *HMSGp2* (SEQ ID NO: 15); or at least 84% sequence identity with residues 2821-3072 of *HMSG35* (SEQ ID NO: 13); and wherein at least one oligonucleotide primer hybridizes to residues 2794-2886 of *HMSGp1* (SEQ

Cl1 cancel ID NO: 1), 2758-2850 of *HMSGp3* (SEQ ID NO: 3), 2845-2937 of *HMSG11* (SEQ ID NO: 5), 2839-2931 of *HMSG14* (SEQ ID NO: 7), 2836-2928 of *HMSG32* (SEQ ID NO: 9), 2809-2901 of *HMSG33* (SEQ ID NO: 11), 2821-2913 of *HMSG35* (SEQ ID NO: 13), or 1-93 of *HMSGp2* (SEQ ID NO: 15).

2. (**reiterated**) The method according to claim 1, wherein amplification of the human-*P. carinii* nucleic acid sequence is by polymerase chain reaction.

Cl2 3. (**twice amended**) The method of claim 1, wherein the oligonucleotide primers hybridize under low stringency conditions comprising 50°C in 6x SSC, 5x Denhardt's solution, 0.5% SDS and 100 µg sheared salmon testes DNA.

4. (**twice amended**) The method of claim 1, wherein the highly conserved region comprises a sequence selected from the group consisting of: residues 2794-3042 of *HMSGp1* (SEQ ID NO: 1), 2758-3006 of *HMSGp3* (SEQ ID NO: 3), 2845-3090 of *HMSG11* (SEQ ID NO: 5), 2839-3084 of *HMSG14* (SEQ ID NO: 7), 2836-3081 of *HMSG32* (SEQ ID NO: 9), 2809-3054 of *HMSG33* (SEQ ID NO: 11), 2821-3072 of *HMSG35* (SEQ ID NO: 13), and 1-249 of *HMSGp2* (SEQ ID NO: 15).

5. (**twice amended**) The method of claim 1, wherein at least one oligonucleotide primer comprises at least 15 contiguous nucleotides from residues 2794-2886 of *HMSGp1* (SEQ ID NO: 1), 2758-2850 of *HMSGp3* (SEQ ID NO: 3), 2845-2937 of *HMSG11* (SEQ ID NO: 5), 2839-2931 of *HMSG14* (SEQ ID NO: 7), 2836-2928 of *HMSG32* (SEQ ID NO: 9), 2809-2901 of *HMSG33* (SEQ ID NO: 11), 2821-2913 of *HMSG35* (SEQ ID NO: 13), or 1-93 of *HMSGp2* (SEQ ID NO: 15).

6. (**twice amended**) The method of claim 1, wherein at least one oligonucleotide primer comprises at least 15 contiguous nucleotides having at least 91% sequence homology with approximately the same number of nucleotides of residues 2794-2886 of *HMSGp1* (SEQ ID NO: 1), 2758-2850 of *HMSGp3* (SEQ ID NO: 3), 2845-2937 of *HMSG11* (SEQ ID NO: 5), 2839-2931 of *HMSG14* (SEQ ID NO: 7), 2836-2928 of *HMSG32* (SEQ ID NO: 9), 2809-2901 of

HMSG33 (SEQ ID NO: 11), 2821-2913 of *HMSG35* (SEQ ID NO: 13), or 1-93 of *HMSGp2* (SEQ ID NO: 15).

Cl2 amd

7. (**twice amended**) The method of claim 1, wherein at least one oligonucleotide primer comprises at least 15 contiguous nucleotides having at least 95% sequence homology with approximately the same number of nucleotides of residues 2794-2886 of *HMSGp1* (SEQ ID NO: 1), 2758-2850 of *HMSGp3* (SEQ ID NO: 3), 2845-2937 of *HMSG11* (SEQ ID NO: 5), 2839-2931 of *HMSG14* (SEQ ID NO: 7), 2836-2928 of *HMSG32* (SEQ ID NO: 9), 2809-2901 of *HMSG33* (SEQ ID NO: 11), 2821-2913 of *HMSG35* (SEQ ID NO: 13), or 1-93 of *HMSGp2* (SEQ ID NO: 15).

Cl3

8. (**amended**) The method of claim 1, wherein the oligonucleotide primers hybridize under stringent conditions comprising 65°C in 6x SSC, 5x Denhardt's solution, 0.5% SDS and 100 µg sheared salmon testes DNA.

9. (**amended**) The method of claim 1, wherein the oligonucleotide primers consist of one upstream primer and one downstream primer.

10. (**amended**) The method of claim 9, wherein:
the upstream primer is SEQ ID NO: 17, or SEQ ID NO: 18; and
the downstream primer is SEQ ID NO: 20 or SEQ ID NO: 24.

11. (**amended**) The method of claim 1, wherein one of the oligonucleotide primers comprises SEQ ID NO: 17.

12. (**amended**) The method of claim 1, wherein one of the oligonucleotide primers comprises SEQ ID NO: 18.

13. (**amended**) The method of claim 1, wherein one of the oligonucleotide primers comprises SEQ ID NO: 19.

C13 cancel

14. (**amended**) The method of claim 1, wherein one of the oligonucleotide primers comprises SEQ ID NO: 20.

15. **Please cancel claim 15.**

C14

16. (**amended**) The method of claim 1, wherein one of the oligonucleotide primers comprises SEQ ID NO: 24.

17. (**amended**) The method of claim 1, wherein the specimen is from the oropharyngeal tract.

18. (**amended**) The method of claim 1, wherein the specimen is from blood.

19. (**reiterated**) The method of claim 1, wherein the step of determining whether an amplified sequence is present comprises one or more of:

(a) electrophoresis and staining of the amplified sequence; or

(b) hybridization to a labeled probe of the amplified sequence.

20. (**reiterated**) The method of claim 19, wherein the amplified sequence is detected by hybridization to a labeled probe.

C15

21. (**amended**) The method of claim 20, wherein the labeled probe comprises a detectable non-isotopic label chosen from the group consisting of:

a fluorescent molecule;

a chemiluminescent molecule;

an enzyme;

a co-factor;

an enzyme substrate; and

a hapten.

C15 cancel

22. (**amended**) The method of claim 20, wherein the labeled probe comprises SEQ ID NO: 19.

23. (**amended**) A method of detecting the presence of *Pneumocystis carinii* in a human biological specimen, comprising:

exposing the specimen to a probe that hybridizes under stringent conditions to a human-*P. carinii* nucleic acid sequence, if the sequence is present in the specimen, to form a hybridization complex; and

determining whether the hybridization complex is present,

wherein the human-*P. carinii* nucleic acid sequence is *HMSGp1* (SEQ ID NO: 1), *HMSGp3* (SEQ ID NO: 3), *HMSG11* (SEQ ID NO: 5), *HMSG14* (SEQ ID NO: 7), *HMSG32* (SEQ ID NO: 9), *HMSG33* (SEQ ID NO: 11), *HMSG35* (SEQ ID NO: 13), or *HMSGp2* (SEQ ID NO: 15); and

wherein the stringent conditions of hybridization comprise 65°C in 6x SSC, 5x Denhardt's solution, 0.5% SDS and 100 μg sheared salmon testes DNA.

24. (**amended**) The method of claim 23, wherein the probe comprises SEQ ID NO: 19.

Please add the following new claims:

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~~25.~~ (**new**) The method of claim 23, wherein the probe is a labeled probe.

~~26.~~ (**new**) The method of claim 1, wherein two or more of the oligonucleotide primers each comprise at least 15 contiguous nucleotides having at least 91% sequence homology with approximately the same number of nucleotides of residues 2794-2886 of *HMSGp1* (SEQ ID NO: 1), 2758-2850 of *HMSGp3* (SEQ ID NO: 3), 2845-2937 of *HMSG11* (SEQ ID NO: 5), 2839-2931 of *HMSG14* (SEQ ID NO: 7), 2836-2928 of *HMSG32* (SEQ ID NO: 9), 2809-2901 of *HMSG33* (SEQ ID NO: 11), 2821-2913 of *HMSG35* (SEQ ID NO: 13), or 1-93 of *HMSGp2* (SEQ ID NO: 15).

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~~27.~~ (**new**) The method of claim 1, wherein two or more of the oligonucleotide primers each comprise at least 15 contiguous nucleotides having at least 95% sequence homology with

cl 4 cont'd

approximately the same number of nucleotides of residues 2794-2886 of *HMSGp1* (SEQ ID NO: 1), 2758-2850 of *HMSGp3* (SEQ ID NO: 3), 2845-2937 of *HMSG11* (SEQ ID NO: 5), 2839-2931 of *HMSG14* (SEQ ID NO: 7), 2836-2928 of *HMSG32* (SEQ ID NO: 9), 2809-2901 of *HMSG33* (SEQ ID NO: 11), 2821-2913 of *HMSG35* (SEQ ID NO: 13), or 1-93 of *HMSGp2* (SEQ ID NO: 15).

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28. (**new**) The method of claim 1, wherein two or more oligonucleotide primers each comprise at least 15 contiguous nucleotides from residues 2794-2886 of *HMSGp1* (SEQ ID NO: 1), 2758-2850 of *HMSGp3* (SEQ ID NO: 3), 2845-2937 of *HMSG11* (SEQ ID NO: 5), 2839-2931 of *HMSG14* (SEQ ID NO: 7), 2836-2928 of *HMSG32* (SEQ ID NO: 9), 2809-2901 of *HMSG33* (SEQ ID NO: 11), 2821-2913 of *HMSG35* (SEQ ID NO: 13), or 1-93 of *HMSGp2* (SEQ ID NO: 15).

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29. (**new**) The method of claim 4, wherein two or more of the oligonucleotide primers hybridize to residues 2794-2886 of *HMSGp1* (SEQ ID NO: 1), 2758-2850 of *HMSGp3* (SEQ ID NO: 3), 2845-2937 of *HMSG11* (SEQ ID NO: 5), 2839-2931 of *HMSG14* (SEQ ID NO: 7), 2836-2928 of *HMSG32* (SEQ ID NO: 9), 2809-2901 of *HMSG33* (SEQ ID NO: 11), 2821-2913 of *HMSG35* (SEQ ID NO: 13), or 1-93 of *HMSGp2* (SEQ ID NO: 15).

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30. (**new**) The method of claim 29, wherein the oligonucleotide primers hybridize under low stringency conditions comprising 50°C in 6x SSC, 5x Denhardt's solution, 0.5% SDS and 100 µg sheared salmon testes DNA.

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31. (**new**) The method of claim 29, wherein the oligonucleotide primers hybridize under stringent conditions comprising 65°C in 6x SSC, 5x Denhardt's solution, 0.5% SDS and 100 µg sheared salmon testes DNA.

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32. (**new**) A method of detecting the presence of *Pneumocystis carinii* in a human biological specimen, comprising: